

Figure 1

hDEC2a

DEC1

MDEGIPHLQERQ—L——LEHRDFIGLDYSSLYMC-KPKRSMKRQ-DTKDTYKLPHRLIEKKRRDRIN 61
M-ERIPSAQPPPACLPKAPGLEHGDLPGMYPAHMYQVYKSRRGIKRSEDSKETYKLPHRLIEKKRRDRIN 69

ECIAQLKDLLPEHLKLTLGHLEKAVVLETLKHLKALTALTEQQHQKIIALQNG---ERSLKSPIQSD 127
ECIAQLKDLLPEHLKLTLGHLEKAVVLETLKHKVKTNLIDQQQQKIIALQSGLQAGELSGR-NVETG 138

LDAFHSGFQTCAKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGA---PS 194
QEMFCSGFQTCAREVVLQYLAHEN-T-RDLKSSQLVTHLHRVSELLQQGTSRKPSDAPKVMDFKEKPS 206

A-A-GSAAAPCLERAGQKLEPLAYCVPVIQRTQP-SAELAAENDTDTSGYGGEAEPD-R-E---K- 254
SPAAGSEG-P---G-K---N---CVPVIQRTFAHSSGEQSGSDTDTSGYGGESEKG-DLRSEQPCFKS 263

—GK—GAGASRVTIKQEPPGEDSPAPK-RMKL-DSRGGG-SGGGPGGGAAAAAAALLGPDAAAALLR 317
DHGRRFTMGERIGAIKQESE-E-PPTKKNRMQLSDDEGHFTSS—D— 305

PDAALLSSLVAFGGGGAPFP-QPAAAAPFCLPFCFLSP-SAAAAYVQFLOKSGLEKYLYPAAAAPF 385
—LISS—PFLG—PHPHQP—PFCLPF-YLIPPSATA-YL-PML—EKCWYPTSV—P— 349

PLLYPGIPAPAAAAAAAAAAFPCLSSVLSPPPKEAGAAATLL-PHEVAPLGAPHQPHGRTH 454
VL-YPGLNASAAA—LSSFMNP—DKISA—PLLMPQR—L—PSP— 385

LPFAGPREPGNPESSA—QE—DPSQPGK—EA—P 482
LP-AHP—SVDSSVLLQALKPIPPLNLETKD

(Homology 43%)

Figure 2

hDEC2a

hDEC2b

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTK--DTYKLPHRLIEKKRRDRINECIAQLK 68

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKVSDTYKLPHRLIEKKRRDRINECIAQLK 70

DLLPEHLKLTTLGHLEKAVVLETLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTC 138

DLLPEHLKLTTLGHLEKAVVLETLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLDAFHSGFQTC 140

AKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 208

AKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 210

QKLEPLAYCVPVIQRTQPSAELAAENDTDSGYGEAARPDRKGKGAGASRVTIKQEPPGEDSPAPK 278

QKLEPLAYCVPVIQRTQPSAELAAENDTDSGYGEAARPDRKGKGAGASRVTIKQEPPGEDSPAPK 280

RMKLDsRGGSGGPGGGAAAAAALLGPDPAAAALLRPDAALLSSLVAFGGGGAPFPQPAAAAPFC 348

RMKLDsRGGSGGPGGGAAAAAALLGPDPAAAALLRPDAALLSSLVAFGGGGAPFPQPAAAAPFC 350

LPFCFLSPSAAAAYQPFLDKSGLEKYLYPAAAAPFPLLYPGIPAPAAAAAAAAAFPCLSSV 418

LPFCFLSPSAAAAYQPFLDKSGLEKYLYPAAAAPFPLLYPGIPAPAAAAAAAAAFPCLSSV 420

LSPPPEKAGAAAATLLPHEVAPLGAPHQPHGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP 482

LSPPPEKAGAAAATLLPHEVAPLGAPHQPHGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP 484

Figure 3

hDEC2a

mDEC2a

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKDTYKLPHRLIEKKRRDRINECIAQLKDL 70

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRDRTKDTYKLPHRLIEKKRRDRINECIAQLKDL 70

LPEHLKLTLGHLEKAVVLETLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSQDAFHSGFQTCAK 140

LPEHLKLTLGHLEKAVVLETLKHLKALTALTEQQHQKIIALQNGERSLKSIVQADLDAFHSGFQTCAK 140

EVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSK-GTG-AP-SAAGSAAAPCLERA 207

EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ—VP-SGRGSGRAPCSA-G-AAA—A 196

-GQKLEPLAYCVPVIQRTQPSAELAAENDTDTSGYGGEAEPDREKGKGAGASRVTIKQEPPGEDS-P 275

SGP—ERVARCVPIQRTQPGTEP—EHDTDSDGYGGEAE-QG-R—A-A—V—KQEPPG-DSSP 249

APKRMKLDRGGGGGGGGGGGAAAAAAALLGPDPAAAALLRPDAALLSSLVAFGGGGAPFPQPAAAAA 345

APKRPKLEARG—ALLGPEPA—LL—G—SLVAL—GGGAPFAQPAAA— 288

PFCLPFCFLSPSAAAAYVQFLDKSGLEKYLYPAAAAPFPILYPGIPAPAAAAAAAAAAFPCL 415

PFCLPFYLLSPSAAA-YVQPWLDKSGLDKYLYPAAA-PFPILYPGIPA—AAAAAAAAPCL 348

SSVLSPPEKAGA-AAATLLPHEVAPLGAP-HPQHPHGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP 482

SSVLSPPEKAGATAGAPFLAHEVAPPG-PLRPQHHSRTHLPRAV—NPESS-QEDATQPAKDAP 410

Figure 4

hDEC2a

mDEC2a

SHARP-1

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKDTYKLPFHRLIEKKRRDRINECIAQLKDL 70

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRDRTKDTYKLPFHRLIEKKRRDRINECIAQLKDL 70

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRDRTKDTYKLPFHRLIEKKRRDRINECIAQLKDL 70

LPEHLKLTTLGHLEKAVVLETLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDDAFHSGFQTCAK 140

LPEHLKLTTLGHLEKAVVLETLKHLKALTALTEQQHQKIIALQNGERSLKSPVQADLDAFHSGFQTCAK 140

LPEHLKLTTLGHLEKAVVLETLKHLKALTALTEQQHQKIIALQNGERSLKSPVQADLDAFHSGFQTCAK 140

EVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQVPLSK-GTG-AP-SAAGSAAAPCLERA 207

EVLQYLFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VP-SGRGSGRAPCSA-G-AAA-----A 196

EVLQYLFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VT-PGRGPGRAPCSA-G-AAA-----A 196

-GQKLEPLAYCVPVIQRTOPSAELAAENDTDTSGYGGEAARPDRKGKGAGASRVTIKQEPPGEDS-P 275

SGP-ERVARCVPVIQRTQPGTEP-EHDTDTSGYGGEAE-QG-R-----A-A-V-KQEPPG-DSSP 249

SGS-ERVARCVPVIQRTQPGTEP-EHDTDTSGYGGEAE-QG-R-----A-A-V-KQEPPG-DPSL 249

APKRMKLDRGGSGGPGGGAAAAAAALLGPAAAALLRPAALLSSLVAFGGGGAPFPQPAAAA 345

APKRPKLEARG-----ALLGPEPA-----LL-----G-----SLVAL-----GGGAPFAQPAAA 288

RPRG

253

PFCLPFCFLSPSAAAAYQPFLDKSGLEKYLYPAAAAPFPLLYPGIPAPAAAAAAAAAAAFPCL 415

PFCLPFYLLSPSAAA-YVQPWLDKSGLDKYLYPAAA-PFPLLYPGIPA-----AAAAAAAAAFPCL 348

SSVLSPPEKAGA-AAATLLPHEVAPLGAP-HPQPHGRTHLPFAGPREPGNPESSAQEDPSQPGKEAP 482

SSVLSPPEKAGATAGAPFLAHEVAPPG-PLRPQHHSRTHLPRAV-----NPESS-QEDATQPAKDAP 410